



PROGRAM ACTIVITY REPORT (PAR)

GENOMIC TECHNIQUES FOR FERAL SWINE EPIDEMIOLOGY

The NWDP conducts feral swine disease surveillance in over 35 states each year. This effort contributes to a better understanding of disease distribution and ultimately the risk diseases pose to the commercial swine industry and human health. The continued spread of feral swine populations across the United States has also resulted in the expansion of endemic feral swine diseases in many areas.

Pseudorabies is currently found in feral swine populations in 26

states whereas swine brucellosis has been documented in 18 states, and these numbers increase each year. These increases may be due to disease expansion by natural transmission mechanisms or by translocation of infected individuals into a previously naïve area. Alternatively, these diseases may have already been established and previous sample sizes were not sufficient to detect their presence.

Disease transmission events between feral swine and free range (or transitional) domestic livestock are similarly difficult to interpret. The

epidemiologists to fine-tune their investigations. Next generation sequencing methods are becoming affordable and provide enough detail to determine likely disease introduction pathways and directionality. Phylogenetic analyses using either whole genome sequencing, multilocus sequence typing (MLST), or multiple-locus [variable number tandem repeat (VNTR)] analysis (MLVA) allow accurate reconstruction of disease transmission histories at relevant scales to inform and direct best management practices.

For an overview of these techniques in the context of swine brucellosis epidemiology, please see:

[Leiser, O.P., J.L. Corn, B.S. Schmit, P.S. Klein, and J.T. Foster. 2013. Feral swine brucellosis in the United States and prospective genomic techniques for disease epidemiology. Veterinary Microbiology 166:1-10.](#)

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PHOTO
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host range and genetic complexity of the disease causing organism may help or hinder epidemiological investigations and ultimately management outcomes. Fortunately, recent advances in genomic techniques allow wildlife

The original artwork on this page was created by the National Wildlife Disease Program's Erika Kampe and Sarah Goff



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